Artificial Intelligence (CS562)

Sequence Alignment

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- To solve the problem of Sequence Alignment, we used the approach of *Best First Search* algorithm on a special weighted grid.

- In SA, we have a randomly generated original sequence of length M, and a modified sequence of length N where $M>N$.

- A grid (weighted graph) is constructed with diagonals going from top left to bottom right and corresponding edge weights depending upon the matching sequence.
  Eg - A–>A = 0, A–>T = 2, A–>G = 4, etc.

- The mutation in the modified sequence depends on the parameter *alpha* which determines how much the sequence has to be mutated.

- A tool bar is present for selection of the values of M (columns), N (rows), alpha, and the original and modified sequence displays.

- The source node is the topmost leftmost node and the goal node is the bottommost rightmost node for the full sequence. Source and goal nodes can be changed depending upon the subsequences we want to test against.

- The path traced by the algorithm from source to goal shows how similar the sequence is by finding the path with least cost.

- Turns in the path away from the diagonal indicate multiple matches and blanks in the modified sequence compared to the original sequence.